

FIGURE 1

Amino acid sequence for full-length human wild type DPPIV [SEQ. ID No.:NO: 1]
(Residues 39-766 are underlined)

MKTPWKVLLG	LLGAAALVTI	ITTPVVLLNK	GTDDATADSR	KTYTLTDYKL	NTYRLKLYSL	60
RWISDHELYK	KQENNLLVFN	AEGNNSVFL	ENSTPDERGH	SINDYSISPD	GOFILLEYNN	120
VKOWRHSYTA	SYDIYDLNKR	OLITEERIPN	NTQWVITWSPV	GHKLAVWNN	DIYVKIEPNL	180
PSYRITWTGK	EDIIYNGIID	WVYEEEVFSA	YSAIWWSPNG	TFLAYAQFND	TEVPLIEYSF	240
YSDESLQYTK	TVRVPYFKAG	AVNPTVKFPV	VNTDLSLSSVT	NATSIQITAP	ASMLIGDHYL	300
CDVITWAQER	ISLQLWLRIQK	MDNSVWMLCDY	DESSGRWNCL	VARQHIEMST	TGWVGRFRPS	360
EPHPTLDGNS	FYKIIISNEEG	YRHICYQFQID	KKDCTPSYD	TWEVIGIEAL	TSDYLYYIISN	420
EVYKGMPPGRN	LYKIQLSDYT	KVTCIISCELN	PERCOVYVS	FSKEAKYQYL	RCSPGPLPLY	480
TLHSSVNDKG	LRVLEDDNSAL	DKMLQNVOMP	SKKLDIIFLN	ETKFWYQMIL	PFHFDKSKKY	540
PFLLSDVYAGP	CSQKADTVFR	LNKRLATLST	ENIIIVASPDG	RGSGYQODK1	MHAIRNRLGTL	600
FEVEDDIEAA	QCFSKMCFGV	NKRILAIWGS	YGGVYTSVML	GSGSGVFKCG	IAVAPVSRWE	660
YYDSVYTERY	MGLPTPEDNL	DHYRNSTVMS	RAENFKQVQEY	LLIHGTADDN	VHFQQSAQIS	720
KALVDVGVD	QAMWYTDEDH	GIASSTARQH	IYTHMHSFIK	QCFSLP		766

Amino acid sequence for residues 39-766 of DPPIV with a
N-terminal 6x-histidine tag [SEQ. ID No.:NO: 3]
(part of a gp67 signal sequence and a 6x-histidine tag is underlined)

ADPGGSHHHH	HHHSRKTYTLT	DYLNKNTYRLK	LYSLRWISDH	EYLYKQENNI	LVFNAEYGN	60
SVFLENSTFD	EEFGHSINDYS	ISPQGQFILL	EYNVVKQWNR	SYTASYDIYD	LNKRQLITEE	120
RIPMNTQWV	WSPVCHKLAY	VWNNDIYVKI	EPNLPSYRIT	WTGKEDIIYN	GITDOWYEEE	180
VFSAYSALWW	SPNGTFLAYA	QFNQDTEVPLI	EYSFYSDESL	QYPKIVRVPY	PKAGAVNPTV	240
KFFVNTDSDL	SSVTNATSIQ	ITAPASMLIG	DHYLCDVTVW	TQERISLQWL	RRIQNYSVMD	300
ICDYDESSGR	WNCLVVARQH	EMSTTGWGR	FRPSEPHPTL	DGNSFYKIIIS	NEEGYRHYIC	360
FQIDKKDCTF	ITKGTWVIG	IRALTSIDYL	YISNEYKGM	GGRNLYKIQL	SDYTKVTCLS	420
CELNPERCQY	YVSFSKEAK	YYQLRCGSPG	LPLYTLHSSV	NDKGLRVLLED	NSALDKMLQN	480
VQMPSKKDF	IILNETKFW	QMLPFPFDK	SKKYPPLLVD	YAGPCSQKAD	TVFRLNWATY	540
LASTENIIVA	SFDGRGSQYQ	GDKIMHAINR	RLGTFEVEDQ	IEAARQFSKM	GPVDNKRIAI	600
NGWSYGGVYI	SMVLGSGSGV	FKCGIAVAPV	SRWEYYDSVY	TERYMLPTP	EDNLDHYRNS	660
TVMSRAENFK	QVEYLLIHTG	ADDNVHFQQS	AQISKALVVD	GVDFQAMWYT	DEDHGIASST	720
AHQHIIYTHMS	HFIKQCFSLP					740

FIGURE 1 (Cont.)A

Human cDNA sequence encoding residues 39-766 of DPPIV [SEQ_ID No. 2 NO: 3]

AGTCGCAAAA CTTACACTCT AACTGATTAC TAAAAAATA CTTATAGACT GAAGTTTATAC 60
 TCCCTTAAGAT GGATTTCAGA TCATGAATAT CTCTACAAAC AAGAAAATAA TATCTTGGTA 120
 TTCAATGCTG AATATGGAAA CAGCTCAGTT TTCTTGGAGA ACAGTACATT TGATGAGTT 180
 GGACATTCTA TCAATGATTA TTCAATATCT CCGATGTTGG AGTTTATTCT TTAGAATAC 240
 AACTACGTGA AGCAATGGAG GCATTCTCAAC ACAGCTTCAAT AGACATTTA TATTTAAAT 300
 AAAAGGCAGC TGATTAACAGA AGAGGAAATT CCAAACAAACCA CACAGTGGGT CACATGGTCA 360
 CCACGGGTC ATAATATTGGC ATATGTTGGC AACAATGACA TTTATGTTAA AATTGAACCA 420
 AATTTACCAA GTTACAGATC CACATGGACG GGGAAAGAAG ATATAATATA TAATGGATA 480
 ACTGAGTGGG TTATGAGA GGAAGCTCTG AGTGCCTACT CTGCTCTGTG GTGGTCTCCA 540
 AACCGCAACTT TTATGAGATA CGCCCAATTAA ACAGCACACAG AAGTCCCACT TATTGAATAC 600
 TCCCTTCACT CTGATGACTC ACTGCGTAC CCAAAGACTG TACCGGTTCC ATATCCAAG 660
 GCAGGAGCTC TGAATCCAC TGTAAGCTG TTGTTGTTAA ATACAGACTC TCTCAGCTCA 720
 GTCCACCATG CAACTCTCATC ACAAATCACT GCTCTGCTT CTATGTTGAT AGGGGATCAC 780
 TACTTGTGTT ATGTGACATG CGAACACACAA GAAAGAATTT CTTTGCAGTGG GCTCAGGAGG 840
 ATTCAAGACT ATTCGCTGTG GGATATTGTT GACTATGATG AAATCCAGTG AGATGGAAC 900
 TGCTTAGTGG CACGGCAACAA CATTGAAATG AGTACTACTG GCTGGTTGG AAGATTAGG 960
 CCTCTATACCT CTCATTCTG CTTGTGATG ATAGCTCTT ACAGATCAT CAGCAATGAA 1020
 GAAGGTTACA GACACATTG CTATTTCCAA ATAGATAAAAA AAAGACTGCACT ATTTTATACA 1080
 AAAGGCACCT GGGAAAGTCAT CGGGATAGAA GCTCTAACCA GTGATTATCT ATACTACATT 1140
 AGTAATGAAAT ATAAAGGATG GCCAGGAGGA AGGAATCTTT ATAAATATCCTC ACTTATTGAC 1200
 TATAACAAAG TGACATGCTC CAGTTGATG CTGAAATCCG AAAGGTTGTC GTRACTATCTC 1260
 GTGTCAATCA CTAAAGGAGGC GAAGTATTATG CAGCTGAGAT GTTCCGGTCC TGGTCTGCC 1320
 CTCTATACCTC TACACAGCAG CGTGTGATG AAAGGGCTGA GACTCTGGA AGACAATTC 1380
 GCTTTGGATA AAATGCTGCA GAATGTCGCA ATGCCCCCTCA AAAACTGGA CTTCATTAATT 1440
 TTGAATGAAA CAAATTTTG GTATCAGATG ATCTTGGCTC CTCATTTGAA TAAATCCAAAG 1500
 AAATATCCTC TACTATTAGA TGTCATGCA CGCCCATGTA GTCAAAAAGC AGACACTGTC 1560
 TTCAGACTGA ACTGGGCCAC TTACCTTGCA AGCACAGAAA ACATTATAGT AGCTAGCTT 1620
 GATGGCAGAG GAAGTGGTTA CCAAGGAGAT AGATCATGCA ATGCAATCCTA CAGAAAGACTG 1680
 GGAACATTG AAGTGAAGA TCAAAATTGAA GCAGCCAGAC AATTTCCTAA AATGGGATT 1740
 GTGGACAAACA AACGAATTGTC ATTGGGGTC TGGTCATGAT GAGGGTACGT AACCTCAATG 1800
 GTCTCTGGGT CGGGAAATGG CGTGTGTCAG TGTTGATAGC CGCTGGCCGC TGATATCCCG 1860
 TGGGAGTACT ATGACTCAGT GTACACAGAGA CGTTCATGG GTCTCCCAAC TCCAGAAAGAC 1920
 AACCTTGACCA ATTACAGAAA TTCAACAGTC ATGAGCAGAG CTGAAAATT TAAACAAAGTT 1980
 GAGTACCTCC TTATTCATGG AACAGCAGAT GATAACGTTT ACCTTCAGCA GTCAAGCTCAG 2040
 ATCTCCAAAG CCCTGGTCGA TTGTTGGAGTG GATTTCCAGG CAATGTGGTA TACTGTGAA 2100
 GACCATGGAA TAGCTAGCAG CACAGCACAC CAACATATAT ATACCCACAT GAGCCACCTC 2160
 ATAAACCATG GTTCTCTT ACCT 2184

FIGURE 3

LEGEND

Column headings from left to right are (A)'Atom Number', (B)'Atom Type', (C)'Amino Acid', (D)'Chain Identifier', (E)'Amino Acid Number' (reference to SEQ ID NO: 3), (F)'X Coordinate', (G)'Y Coordinate', (H)'Z Coordinate', (I)'Occupancy' (OCC) and (J)'B factor'.

A	B	C	D	E	F	G	H	I	J
1	N	ARG A	5214		-78.499	25.732	64.898	1.00	51.08
2	CA	ARG A	5214		-77.682	24.936	63.934	1.00	50.91
3	CB	ARG A	5214		-76.853	25.895	63.064	1.00	51.59
4	CG	ARG A	5214		-76.507	25.382	61.666	1.00	54.33
5	CD	ARG A	5214		-76.170	26.503	60.678	1.00	58.00
6	NE	ARG A	5214		-76.489	26.159	59.292	1.00	61.47
7	CZ	ARG A	5214		-76.158	26.909	58.245	1.00	62.24
8	NH1	ARG A	5214		-75.492	28.043	58.429	1.00	61.77
9	NH2	ARG A	5214		-76.486	26.525	57.016	1.00	62.51
10	C	ARG A	5214		-76.763	23.943	64.655	1.00	49.68
11	O	ARG A	5214		-75.871	23.360	64.038	1.00	49.98
12	N	LYS A	5315		-76.986	23.740	65.952	1.00	47.84
13	CA	LYS A	5315		-76.093	22.892	66.731	1.00	46.49
14	CB	LYS A	5315		-75.983	23.350	68.181	1.00	46.98
15	CG	LYS A	5315		-77.288	23.731	68.859	1.00	49.99
16	CD	LYS A	5315		-77.002	24.390	70.224	1.00	53.43
17	CE	LYS A	5315		-78.085	25.406	70.605	1.00	55.57
18	NZ	LYS A	5315		-77.642	26.378	71.671	1.00	57.35
19	C	LYS A	5315		-76.358	21.398	66.670	1.00	44.72
20	O	LYS A	5315		-77.487	20.943	66.476	1.00	44.71
21	N	THR A	5416		-75.279	20.641	66.812	1.00	42.33
22	CA	THR A	5416		-75.363	19.201	66.815	1.00	39.34
23	CB	THR A	5416		-74.225	18.582	66.009	1.00	39.46
24	OG1	THR A	5416		-72.972	18.975	66.565	1.00	38.25
25	CG2	THR A	5416		-74.187	19.163	64.603	1.00	38.11
26	C	THR A	5416		-75.295	18.761	68.251	1.00	37.67
27	O	THR A	5416		-75.098	19.578	69.150	1.00	37.00
28	N	TYR A	5517		-75.534	17.476	68.466	1.00	35.46
29	CA	TYR A	5517		-75.439	16.896	69.785	1.00	33.88
30	CB	TYR A	5517		-76.340	15.666	69.865	1.00	33.82
31	CG	TYR A	5517		-76.311	14.944	71.179	1.00	32.28
32	CD1	TYR A	5517		-77.203	15.265	72.191	1.00	32.55
33	CE1	TYR A	5517		-77.170	14.603	73.411	1.00	32.32
34	CZ	TYR A	5517		-76.248	13.588	73.600	1.00	31.27
35	OH	TYR A	5517		-76.199	12.905	74.782	1.00	29.92
36	CE2	TYR A	5517		-75.366	13.257	72.606	1.00	30.87
37	CD2	TYR A	5517		-75.395	13.936	71.406	1.00	30.90
38	C	TYR A	5517		-73.971	15.626	69.924	1.00	32.90
39	O	TYR A	5517		-73.501	15.626	69.247	1.00	32.98
40	N	THR A	5618		-73.247	17.244	70.776	1.00	31.58
41	CA	THR A	5618		-71.792	17.060	70.901	1.00	30.40

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FIGURE 3-(Cont.)A

A	B	C	D	E	F	G	H	I	J
42	CB	THR A	5618		-71.126	18.369	71.311	1.00	29.92
43	OG1	THR A	5618		-71.551	18.690	72.644	1.00	29.95
44	CG2	THR A	5618		-71.606	19.526	70.444	1.00	30.35
45	C	THR A	5618		-71.353	16.053	71.937	1.00	29.51
46	O	THR A	5618		-72.131	15.625	72.782	1.00	28.96
47	N	LEU A	5719		-70.064	15.739	71.895	1.00	29.18
48	CA	LEU A	5719		-69.454	14.841	72.858	1.00	29.40
49	CB	LEU A	5719		-67.958	14.681	72.570	1.00	29.30
50	CG	LEU A	5719		-67.186	13.725	73.475	1.00	29.28
51	CD1	LEU A	5719		-67.664	12.278	73.289	1.00	26.89
52	CD2	LEU A	5719		-65.706	13.844	73.171	1.00	29.54
53	C	LEU A	5719		-69.668	15.422	74.247	1.00	29.40
54	O	LEU A	5719		-70.014	14.702	75.174	1.00	29.52
55	N	THR A	5820		-69.483	16.731	74.375	1.00	29.38
56	CA	THR A	5820		-69.674	17.419	75.650	1.00	29.71
57	CB	THR A	5820		-69.270	18.921	75.530	1.00	30.55
58	OG1	THR A	5820		-67.858	19.022	75.275	1.00	31.86
59	CG2	THR A	5820		-69.426	19.646	76.871	1.00	29.63
60	C	THR A	5820		-71.095	17.286	76.152	1.00	29.39
61	O	THR A	5820		-71.311	17.062	77.336	1.00	29.75
62	N	ASP A	5921		-72.070	17.413	75.255	1.00	29.23
63	CA	ASP A	5921		-73.467	17.237	75.640	1.00	28.50
64	CB	ASP A	5921		-74.381	17.347	74.420	1.00	28.92
65	CG	ASP A	5921		-74.390	18.740	73.824	1.00	30.30
66	OD1	ASP A	5921		-74.348	19.699	74.612	1.00	30.33
67	OD2	ASP A	5921		-74.413	18.969	72.588	1.00	31.62
68	C	ASP A	5921		-73.635	15.871	76.288	1.00	28.19
69	O	ASP A	5921		-74.255	15.737	77.363	1.00	27.07
70	N	TYR A	6022		-73.067	14.854	75.635	1.00	28.18
71	CA	TYR A	6022		-73.110	13.498	76.162	1.00	28.06
72	CB	TYR A	6022		-72.478	12.503	75.180	1.00	28.13
73	CG	TYR A	6022		-72.316	11.105	75.757	1.00	28.21
74	CD1	TYR A	6022		-73.381	10.473	76.387	1.00	27.52
75	CE1	TYR A	6022		-73.231	9.225	76.941	1.00	31.17
76	CZ	TYR A	6022		-71.994	8.574	76.850	1.00	31.00
77	OH	TYR A	6022		-71.855	7.320	77.396	1.00	33.09
78	CE2	TYR A	6022		-70.920	9.184	76.231	1.00	27.37
79	CD2	TYR A	6022		-71.086	10.444	75.703	1.00	27.39
80	C	TYR A	6022		-72.400	13.430	77.507	1.00	28.37
81	O	TYR A	6022		-72.966	12.974	78.504	1.00	28.20
82	N	LEU A	6123		-71.160	13.894	77.544	1.00	29.10
83	CA	LEU A	6123		-70.363	13.783	78.766	1.00	29.84
84	CB	LEU A	6123		-68.895	14.060	78.490	1.00	29.67
85	CG	LEU A	6123		-68.233	13.147	77.454	1.00	30.09
86	CD1	LEU A	6123		-66.745	13.421	77.442	1.00	27.93
87	CD2	LEU A	6123		-68.502	11.647	77.730	1.00	29.29
88	C	LEU A	6123		-70.846	14.639	79.919	1.00	30.85
89	O	LEU A	6123		-70.704	14.254	81.081	1.00	31.02
90	N	LYS A	6224		-71.417	15.798	79.613	1.00	31.74
91	CA	LYS A	6224		-71.909	16.658	80.669	1.00	33.11
92	CB	LYS A	6224		-71.501	18.129	80.433	1.00	33.11

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FIGURE 3-(Cont.)B

A	B	C	D	E	F	G	H	I	J
93	CG	LYS A	6224		-69.997	18.373	80.362	1.00	31.71
94	CD	LYS A	6224		-69.297	17.906	81.648	1.00	32.14
95	CE	LYS A	6224		-67.820	18.355	81.702	1.00	32.14
96	NZ	LYS A	6224		-67.002	17.666	82.769	1.00	29.53
97	C	LYS A	6224		-73.426	16.521	80.864	1.00	34.49
98	O	LYS A	6224		-73.998	17.135	81.752	1.00	34.44
99	N	ASN A	6225		-74.082	15.701	80.048	1.00	36.12
100	CA	ASN A	6225		-75.517	15.506	80.214	1.00	37.50
101	CB	ASN A	6225		-75.813	14.898	81.583	1.00	38.04
102	CG	ASN A	6225		-75.397	13.437	81.686	1.00	42.36
103	OD1	ASN A	6225		-75.195	12.919	82.793	1.00	46.50
104	ND2	ASN A	6225		-75.285	12.753	80.534	1.00	46.18
105	C	ASN A	6225		-76.312	16.808	80.032	1.00	37.71
106	O	ASN A	6225		-77.122	17.187	80.870	1.00	37.63
107	N	THR A	6426		-76.066	17.493	78.926	1.00	38.29
108	CA	THR A	6426		-76.761	18.725	78.622	1.00	38.88
109	CB	THR A	6426		-76.259	19.227	77.281	1.00	39.01
110	OG1	THR A	6426		-74.854	19.444	77.377	1.00	39.58
111	CG2	THR A	6426		-76.817	20.607	76.955	1.00	39.02
112	C	THR A	6426		-78.271	18.476	78.551	1.00	39.19
113	O	THR A	6426		-79.066	19.157	79.198	1.00	39.04
114	N	TYR A	6527		-78.637	17.482	77.754	1.00	39.58
115	CA	TYR A	6527		-80.017	17.110	77.518	1.00	39.93
116	CB	TYR A	6527		-80.169	16.771	76.044	1.00	39.52
117	CG	TYR A	6527		-79.698	17.921	75.211	1.00	38.77
118	CD1	TYR A	6527		-80.438	19.087	75.151	1.00	39.35
119	CE1	TYR A	6527		-80.006	20.166	74.431	1.00	39.27
120	CZ	TYR A	6527		-78.817	20.093	73.765	1.00	38.78
121	OH	TYR A	6527		-78.400	21.180	73.049	1.00	38.94
122	CE2	TYR A	6527		-78.051	18.947	73.817	1.00	38.83
123	CD2	TYR A	6527		-78.488	17.878	74.549	1.00	38.20
124	C	TYR A	6527		-80.398	15.926	78.368	1.00	40.73
125	O	TYR A	6527		-80.207	14.793	77.969	1.00	41.03
126	N	ARG A	6628		-80.940	16.177	79.546	1.00	42.07
127	CA	ARG A	6628		-81.271	15.065	80.420	1.00	43.55
128	CB	ARG A	6628		-81.423	15.521	81.873	1.00	44.02
129	CG	ARG A	6628		-80.996	14.454	82.878	1.00	47.22
130	CD	ARG A	6628		-81.354	14.734	84.340	1.00	51.56
131	NE	ARG A	6628		-82.668	14.202	84.699	1.00	55.65
132	CZ	ARG A	6628		-83.559	14.845	85.448	1.00	57.92
133	NH1	ARG A	6628		-83.291	16.050	85.930	1.00	58.60
134	NH2	ARG A	6628		-84.725	14.279	85.715	1.00	60.08
135	C	ARG A	6628		-82.534	14.355	79.951	1.00	43.77
136	O	ARG A	6628		-83.352	14.918	79.221	1.00	44.23
137	N	LEU A	6729		-82.669	13.097	80.338	1.00	43.66
138	CA	LEU A	6729		-83.883	12.376	80.054	1.00	43.77
139	CZ	LEU A	6729		-83.602	10.950	79.602	1.00	43.85
140	CG	LEU A	6729		-83.293	10.758	78.121	1.00	44.26
141	CD1	LEU A	6729		-82.836	9.324	77.850	1.00	45.40
142	CD2	LEU A	6729		-84.505	11.088	77.282	1.00	45.47
143	C	LEU A	6729		-84.578	12.376	81.381	1.00	43.80

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FIGURE 3-(Cont.)C

A	B	C	D	E	F	G	H	I	J
144	O	LEU	A	6729	-83.983	12.028	82.397	1.00	43.27
145	N	LYS	A	6830	-85.831	12.804	81.393	1.00	43.83
146	CA	LYS	A	6830	-86.540	12.864	82.653	1.00	44.19
147	CB	LYS	A	6830	-87.558	13.999	82.623	1.00	44.45
148	CG	LYS	A	6830	-87.589	14.791	83.904	1.00	45.86
149	CD	LYS	A	6830	-87.585	16.278	83.631	1.00	48.33
150	CE	LYS	A	6830	-87.850	17.057	84.915	1.00	50.36
151	NZ	LYS	A	6830	-87.184	16.414	86.093	1.00	50.63
152	C	LYS	A	6830	-87.188	11.530	82.992	1.00	43.80
153	O	LYS	A	6830	-87.671	10.828	82.119	1.00	43.69
154	N	LEU	A	6931	-87.176	11.182	84.269	1.00	43.81
155	CA	LEU	A	6931	-87.756	9.930	84.734	1.00	43.79
156	CB	LEU	A	6931	-86.736	9.163	85.574	1.00	43.75
157	CG	LEU	A	6931	-85.603	8.328	84.969	1.00	44.56
158	CD1	LEU	A	6931	-84.873	9.055	83.846	1.00	43.44
159	CD2	LEU	A	6931	-84.628	7.930	86.096	1.00	44.48
160	C	LEU	A	6931	-88.977	10.156	85.617	1.00	43.68
161	O	LEU	A	6931	-89.333	11.277	85.963	1.00	43.78
162	N	TYR	A	7032	-89.615	9.065	85.996	1.00	43.53
163	CA	TYR	A	7032	-90.674	9.138	86.968	1.00	43.23
164	CB	TYR	A	7032	-92.052	9.303	86.338	1.00	43.05
165	CG	TYR	A	7032	-93.048	9.809	87.349	1.00	42.24
166	CD1	TYR	A	7032	-93.511	8.981	88.365	1.00	40.80
167	CE1	TYR	A	7032	-94.404	9.431	89.295	1.00	40.31
168	CZ	TYR	A	7032	-94.844	10.741	89.243	1.00	41.67
169	OH	TYR	A	7032	-95.739	11.185	90.191	1.00	43.57
170	CE2	TYR	A	7032	-94.393	11.593	88.260	1.00	41.02
171	CD2	TYR	A	7032	-93.490	11.127	87.321	1.00	41.49
172	C	TYR	A	7032	-90.607	7.874	87.767	1.00	43.22
173	O	TYR	A	7032	-91.398	6.966	87.573	1.00	43.16
174	N	SER	A	7133	-89.646	7.823	88.671	1.00	43.72
175	CA	SER	A	7133	-89.442	6.642	89.486	1.00	44.29
176	CB	SER	A	7133	-87.971	6.494	89.860	1.00	44.28
177	OG	SER	A	7133	-87.829	5.415	90.769	1.00	45.94
178	C	SER	A	7133	-90.255	6.707	90.749	1.00	44.40
179	O	SER	A	7133	-90.016	7.558	91.591	1.00	44.77
180	N	LEU	A	7234	-91.195	5.782	90.895	1.00	44.57
181	CA	LEU	A	7234	-92.057	5.761	92.058	1.00	44.62
182	CB	LEU	A	7234	-93.520	5.959	91.626	1.00	44.14
183	CG	LEU	A	7234	-94.125	4.942	90.643	1.00	43.66
184	CD1	LEU	A	7234	-94.404	3.595	91.314	1.00	40.76
185	CD2	LEU	A	7234	-95.392	5.481	89.957	1.00	41.85
186	C	LEU	A	7234	-91.893	4.444	92.788	1.00	45.36
187	O	LEU	A	7234	-91.354	3.490	92.236	1.00	45.44
188	N	ARG	A	7335	-92.332	4.398	94.038	1.00	46.33
189	CA	ARG	A	7335	-92.342	3.152	94.780	1.00	48.23
190	CB	ARG	A	7335	-91.397	3.171	95.983	1.00	48.19
191	CG	ARG	A	7335	-90.088	3.873	95.758	1.00	50.55
192	CD	ARG	A	7335	-89.158	3.812	96.952	1.00	52.14
193	NE	ARG	A	7335	-87.815	4.235	96.585	1.00	54.13
194	CZ	ARG	A	7335	-86.755	4.134	97.378	1.00	53.95

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FIGURE 3-(Cont.)D

A	B	C	D	E	F	G	H	I	J
195	NH1	ARG	A	7435	-86.886	3.625	98.600	1.00	51.85
196	NH2	ARG	A	7435	-85.569	4.552	96.942	1.00	53.73
197	C	ARG	A	7435	-93.743	3.011	95.297	1.00	48.75
198	O	ARG	A	7435	-94.246	3.909	95.958	1.00	49.28
199	N	TRP	A	7436	-94.381	1.891	95.009	1.00	49.62
200	CA	TRP	A	7436	-95.722	1.668	95.504	1.00	50.47
201	CB	TRP	A	7436	-96.409	0.550	94.751	1.00	50.15
202	CG	TRP	A	7436	-96.845	0.918	93.357	1.00	49.57
203	CD1	TRP	A	7436	-96.282	0.500	92.191	1.00	48.94
204	NE1	TRP	A	7436	-96.956	1.033	91.120	1.00	48.90
205	CE2	TRP	A	7436	-97.985	1.813	91.581	1.00	48.49
206	CD2	TRP	A	7436	-97.945	1.765	92.987	1.00	48.80
207	CE3	TRP	A	7436	-98.902	2.490	93.704	1.00	48.56
208	CZ3	TRP	A	7436	-99.857	3.220	93.005	1.00	49.05
209	CH2	TRP	A	7436	-99.867	3.246	91.607	1.00	47.62
210	CZ2	TRP	A	7436	-98.940	2.553	90.879	1.00	48.27
211	C	TRP	A	7436	-95.581	1.359	96.970	1.00	51.34
212	O	TRP	A	7436	-94.558	0.821	97.388	1.00	51.46
213	N	ILE	A	7537	-96.598	1.685	97.757	1.00	52.47
214	CA	ILE	A	7537	-96.559	1.421	99.191	1.00	53.41
215	CB	ILE	A	7537	-96.449	2.737	99.958	1.00	53.42
216	CG1	ILE	A	7537	-94.987	3.025	100.270	1.00	53.87
217	CD1	ILE	A	7537	-94.196	3.466	99.076	1.00	54.40
218	CG2	ILE	A	7537	-97.246	2.695	101.244	1.00	54.45
219	C	ILE	A	7537	-97.793	0.648	99.612	1.00	53.93
220	O	ILE	A	7537	-97.812	-0.066	100.617	1.00	53.82
221	N	SER	A	7638	-98.833	0.793	98.814	1.00	54.88
222	CA	SER	A	7638	-100.072	0.103	99.078	1.00	55.80
223	CB	SER	A	7638	-101.023	1.013	99.840	1.00	55.67
224	OG	SER	A	7638	-100.863	2.357	99.413	1.00	56.45
225	C	SER	A	7638	-100.650	-0.235	97.731	1.00	56.36
226	O	SER	A	7638	-99.944	-0.241	96.726	1.00	56.35
227	N	ASP	A	7739	-101.945	-0.488	97.696	1.00	57.13
228	CA	ASP	A	7739	-102.560	-0.803	96.435	1.00	57.78
229	CB	ASP	A	7739	-103.718	-1.766	96.627	1.00	58.12
230	CG	ASP	A	7739	-103.988	-2.578	95.392	1.00	59.53
231	OD1	ASP	A	7739	-105.111	-3.106	95.254	1.00	61.71
232	OD2	ASP	A	7739	-103.127	-2.745	94.500	1.00	61.65
233	C	ASP	A	7739	-103.046	0.452	95.753	1.00	57.97
234	O	ASP	A	7739	-103.764	0.363	94.767	1.00	58.27
235	N	HIS	A	7840	-102.660	1.620	96.261	1.00	58.00
236	CA	HIS	A	7840	-103.128	2.865	95.654	1.00	58.81
237	CB	HIS	A	7840	-104.625	3.072	95.920	1.00	59.47
238	CG	HIS	A	7840	-105.071	2.575	97.257	1.00	61.31
239	ND1	HIS	A	7840	-106.098	1.666	97.409	1.00	62.92
240	CE1	HIS	A	7840	-106.264	1.405	98.694	1.00	63.69
241	NE2	HIS	A	7840	-105.379	2.107	99.380	1.00	63.55
242	CD2	HIS	A	7840	-104.618	2.845	98.504	1.00	62.40
243	C	HIS	A	7840	-102.354	4.110	96.059	1.00	58.35
244	O	HIS	A	7840	-102.744	5.229	95.720	1.00	58.06
245	N	GLU	A	7941	-101.259	3.915	96.780	1.00	58.00

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FIGURE 3-(Cont.)E

A	B	C	D	E	F	G	H	I	J
246	CA	GLU	A	9941	-100.409	5.027	97.167	1.00	57.73
247	CB	GLU	A	9941	-100.372	5.162	98.690	1.00	57.77
248	CG	GLU	A	9941	-101.698	5.542	99.334	1.00	57.46
249	CD	GLU	A	9941	-101.505	6.168	100.703	1.00	56.70
250	OE1	GLU	A	9941	-101.106	5.438	101.644	1.00	56.35
251	OE2	GLU	A	9941	-101.736	7.391	100.832	1.00	55.22
252	C	GLU	A	9941	-99.002	4.787	96.645	1.00	57.49
253	O	GLU	A	9941	-98.593	3.642	96.493	1.00	57.77
254	N	TYR	A	9942	-98.256	5.849	96.370	1.00	57.25
255	CA	TYR	A	9942	-96.869	5.669	95.954	1.00	57.17
256	CB	TYR	A	9942	-96.776	5.319	94.471	1.00	56.71
257	CG	TYR	A	9942	-97.027	6.456	93.510	1.00	54.55
258	CD1	TYR	A	9942	-96.053	7.407	93.272	1.00	52.96
259	CE1	TYR	A	9942	-96.254	8.430	92.382	1.00	51.65
260	CZ	TYR	A	9942	-97.440	8.513	91.693	1.00	51.43
261	OH	TYR	A	9942	-97.622	9.545	90.803	1.00	49.55
262	CE2	TYR	A	9942	-98.427	7.572	91.897	1.00	52.02
263	CD2	TYR	A	9942	-98.215	6.546	92.802	1.00	53.03
264	C	TYR	A	9942	-95.948	6.837	96.294	1.00	57.82
265	O	TYR	A	9942	-96.333	8.003	96.191	1.00	57.89
266	N	LEU	A	9943	-94.723	6.510	96.688	1.00	58.48
267	CA	LEU	A	9943	-93.746	7.526	97.049	1.00	59.28
268	CB	LEU	A	9943	-92.773	6.996	98.103	1.00	59.23
269	CG	LEU	A	9943	-93.436	6.643	99.433	1.00	58.97
270	CD1	LEU	A	9943	-92.447	6.044	100.404	1.00	57.55
271	CD2	LEU	A	9943	-94.111	7.874	100.016	1.00	58.52
272	C	LEU	A	9943	-92.975	8.011	95.849	1.00	59.92
273	O	LEU	A	9943	-92.592	7.230	94.989	1.00	60.06
274	N	TYR	A	9944	-92.762	9.318	95.799	1.00	61.07
275	CA	TYR	A	9944	-91.976	9.941	94.749	1.00	62.31
276	CB	TYR	A	9944	-92.881	10.720	93.798	1.00	61.95
277	CG	TYR	A	9944	-92.187	11.345	92.608	1.00	61.54
278	CD1	TYR	A	9944	-91.690	10.561	91.569	1.00	61.21
279	CE1	TYR	A	9944	-91.058	11.136	90.474	1.00	60.70
280	CZ	TYR	A	9944	-90.923	12.508	90.414	1.00	61.23
281	OH	TYR	A	9944	-90.301	13.098	89.336	1.00	61.42
282	CE2	TYR	A	9944	-91.411	13.303	91.433	1.00	60.86
283	CD2	TYR	A	9944	-92.038	12.722	92.516	1.00	61.00
284	C	TYR	A	9944	-91.030	10.867	95.492	1.00	63.51
285	O	TYR	A	9944	-91.299	11.226	96.634	1.00	63.78
286	N	LYS	A	9945	-89.916	11.232	94.873	1.00	65.00
287	CA	LYS	A	9945	-88.948	12.098	95.532	1.00	66.61
288	CB	LYS	A	9945	-87.641	11.335	95.779	1.00	66.63
289	CG	LYS	A	9945	-86.657	12.048	96.701	1.00	67.24
290	CD	LYS	A	9945	-85.319	11.316	96.767	1.00	68.31
291	CE	LYS	A	9945	-84.269	12.139	97.509	1.00	68.73
292	NZ	LYS	A	9945	-84.810	12.690	98.791	1.00	69.48
293	C	LYS	A	9945	-88.702	13.332	94.671	1.00	67.68
294	O	LYS	A	9945	-88.234	13.207	93.540	1.00	67.83
295	N	GLN	A	9946	-89.017	14.518	95.198	1.00	69.00
296	CA	GLN	A	9946	-88.868	15.752	94.415	1.00	70.27

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FIGURE 3-(Cont.)F

A	B	C	D	E	F	G	H	I	J
297	CB	GLN A	8446		-90.210	16.495	94.254	1.00	70.38
298	CG	GLN A	8446		-90.189	17.523	93.118	1.00	71.49
299	CD	GLN A	8446		-91.574	18.038	92.716	1.00	73.94
300	OE1	GLN A	8446		-92.566	17.300	92.755	1.00	74.29
301	NE2	GLN A	8446		-91.637	19.308	92.313	1.00	74.28
302	C	GLN A	8446		-87.771	16.710	94.891	1.00	70.79
303	O	GLN A	8446		-88.012	17.595	95.719	1.00	70.72
304	N	GLU A	8547		-86.569	16.518	94.344	1.00	71.70
305	CA	GLU A	8547		-85.413	17.393	94.580	1.00	72.37
306	CB	GLU A	8547		-85.480	18.608	93.644	1.00	72.68
307	CG	GLU A	8547		-85.040	18.336	92.211	1.00	73.91
308	CD	GLU A	8547		-83.561	18.604	91.986	1.00	75.82
309	OE1	GLU A	8547		-83.116	19.761	92.179	1.00	76.43
310	OE2	GLU A	8547		-82.840	17.657	91.612	1.00	76.92
311	C	GLU A	8547		-85.240	17.869	96.019	1.00	72.44
312	O	GLU A	8547		-84.595	18.894	96.268	1.00	72.64
313	N	ASN A	8648		-85.801	17.116	96.959	1.00	72.46
314	CA	ASN A	8648		-85.737	17.471	98.368	1.00	72.28
315	CB	ASN A	8648		-86.404	18.833	98.599	1.00	72.52
316	CG	ASN A	8648		-85.409	19.943	98.933	1.00	73.27
317	OD1	ASN A	8648		-84.235	19.690	99.213	1.00	74.24
318	ND2	ASN A	8648		-85.890	21.185	98.919	1.00	73.24
319	C	ASN A	8648		-86.443	16.444	99.243	1.00	72.00
320	O	ASN A	8648		-85.861	15.902	100.186	1.00	72.38
321	N	ASN A	8749		-87.695	16.158	98.902	1.00	71.24
322	CA	ASN A	8749		-88.567	15.415	99.796	1.00	70.45
323	CB	ASN A	8749		-89.521	16.417	100.442	1.00	70.52
324	CG	ASN A	8749		-90.018	17.461	99.449	1.00	70.98
325	OD1	ASN A	8749		-90.640	18.460	99.828	1.00	70.94
326	ND2	ASN A	8749		-89.742	17.233	98.166	1.00	70.86
327	C	ASN A	8749		-89.396	14.293	99.200	1.00	69.91
328	O	ASN A	8749		-89.781	14.321	98.028	1.00	70.04
329	N	ILE A	8850		-89.701	13.316	100.042	1.00	69.04
330	CA	ILE A	8850		-90.539	12.205	99.641	1.00	68.26
331	CB	ILE A	8850		-90.337	11.008	100.573	1.00	68.17
332	CG1	ILE A	8850		-88.957	10.390	100.357	1.00	68.29
333	CD1	ILE A	8850		-87.916	10.833	101.355	1.00	68.40
334	CG2	ILE A	8850		-91.408	9.974	100.328	1.00	68.21
335	C	ILE A	8850		-92.001	12.622	99.655	1.00	67.54
336	O	ILE A	8850		-92.544	12.984	100.696	1.00	67.50
337	N	LEU A	8951		-92.628	12.586	98.488	1.00	66.76
338	CA	LEU A	8951		-94.043	12.899	98.366	1.00	65.98
339	CB	LEU A	8951		-94.323	13.580	97.024	1.00	66.02
340	CG	LEU A	8951		-94.640	15.082	97.012	1.00	65.96
341	CD1	LEU A	8951		-93.931	15.820	98.139	1.00	65.12
342	CD2	LEU A	8951		-94.322	15.711	95.652	1.00	65.83
343	C	LEU A	8951		-94.859	11.621	98.471	1.00	65.39
344	O	LEU A	8951		-94.350	10.533	98.225	1.00	65.35
345	N	VAL A	9052		-96.119	11.748	98.869	1.00	64.69
346	CA	VAL A	9052		-97.026	10.608	98.869	1.00	63.91
347	CB	VAL A	9052		-97.772	10.450	100.184	1.00	64.07

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FIGURE 3-(Cont.)G

A	B	C	D	E	F	G	H	I	J
348	CG1	VAL A	9052		-97.047	11.166	101.304	1.00	64.22
349	CG2	VAL A	9052		-98.002	8.966	100.488	1.00	63.60
350	C	VAL A	9052		-98.082	10.913	97.839	1.00	63.33
351	O	VAL A	9052		-98.626	12.013	97.823	1.00	63.43
352	N	PHE A	9153		-98.383	9.949	96.981	1.00	62.56
353	CA	PHE A	9153		-99.390	10.165	95.959	1.00	61.64
354	CB	PHE A	9153		-98.778	10.047	94.569	1.00	61.67
355	CG	PHE A	9153		-98.025	11.265	94.117	1.00	61.05
356	CD1	PHE A	9153		-96.751	11.523	94.586	1.00	61.29
357	CE1	PHE A	9153		-96.053	12.634	94.151	1.00	61.02
358	CZ	PHE A	9153		-96.625	13.495	93.236	1.00	60.95
359	CE2	PHE A	9153		-97.892	13.244	92.756	1.00	60.57
360	CD2	PHE A	9153		-98.580	12.130	93.192	1.00	60.71
361	C	PHE A	9153		-100.505	9.150	96.078	1.00	61.31
362	O	PHE A	9153		-100.254	7.965	96.304	1.00	61.35
363	N	ASN A	9254		-101.742	9.620	95.960	1.00	60.84
364	CA	ASN A	9254		-102.876	8.717	95.857	1.00	60.32
365	CB	ASN A	9254		-104.179	9.395	96.288	1.00	60.41
366	CG	ASN A	9254		-105.340	8.409	96.429	1.00	60.97
367	OD1	ASN A	9254		-106.103	8.477	97.390	1.00	61.46
368	ND2	ASN A	9254		-105.477	7.493	95.470	1.00	60.70
369	C	ASN A	9254		-102.936	8.393	94.382	1.00	59.76
370	O	ASN A	9254		-102.896	9.295	93.543	1.00	59.60
371	N	ALA A	9955		-103.004	7.115	94.047	1.00	59.38
372	CA	ALA A	9955		-103.065	6.740	92.641	1.00	59.02
373	CB	ALA A	9955		-102.952	5.237	92.488	1.00	59.06
374	C	ALA A	9955		-104.322	7.276	91.937	1.00	58.71
375	O	ALA A	9955		-104.242	7.767	90.816	1.00	58.09
376	N	GLU A	9456		-105.473	7.195	92.598	1.00	58.94
377	CA	GLU A	9456		-106.736	7.646	91.991	1.00	59.29
378	CB	GLU A	9456		-107.930	7.354	92.906	1.00	59.17
379	CG	GLU A	9456		-108.493	5.948	92.791	1.00	59.64
380	CD	GLU A	9456		-109.508	5.794	91.670	1.00	59.62
381	OE1	GLU A	9456		-109.458	6.558	90.681	1.00	59.64
382	OE2	GLU A	9456		-110.371	4.904	91.782	1.00	59.77
383	C	GLU A	9456		-106.787	9.115	91.563	1.00	59.42
384	O	GLU A	9456		-107.172	9.421	90.434	1.00	59.29
385	N	TYR A	9557		-106.388	10.023	92.448	1.00	59.76
386	CA	TYR A	9557		-106.556	11.453	92.162	1.00	60.14
387	CB	TYR A	9557		-107.191	12.151	93.365	1.00	60.19
388	CG	TYR A	9557		-108.191	11.284	94.093	1.00	60.37
389	CD1	TYR A	9557		-109.455	11.059	93.565	1.00	60.93
390	CE1	TYR A	9557		-110.373	10.267	94.226	1.00	60.78
391	CZ	TYR A	9557		-110.030	9.676	95.425	1.00	60.79
392	OH	TYR A	9557		-110.941	8.877	96.072	1.00	60.43
393	CB2	TYR A	9557		-108.775	9.871	95.966	1.00	60.89
394	CD2	TYR A	9557		-107.865	10.677	95.299	1.00	60.70
395	C	TYR A	9557		-105.297	12.200	91.743	1.00	60.44
396	O	TYR A	9557		-105.382	13.286	91.170	1.00	60.16
397	N	GLY A	9558		-104.132	11.630	92.037	1.00	60.85
398	CA	GLY A	9558		-102.881	12.281	91.700	1.00	61.42